SEQUENCE LISTING

<110> University of Maryland, Baltimore
GALEN, James E.

<120> USE OF CLYA HEMOLYSIN FOR EXCRETION OF PROTEINS

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<141> 2001-11-23

<150> US 60/252,516
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atc gaa acc gca gat ggg gca tta gat ctt tat aac aaa tac ctc gac       96
Ile Glu Thr Ala Asp Gly Ala Leu Asp Leu Tyr Asn Lys Tyr Leu Asp
            20                  25                  30

cag gtc atc ccc tgg aag acc ttt gat gaa acc ata aaa gag tta agc      144
Gln Val Ile Pro Trp Lys Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser
        35                  40                  45

cgt ttt aaa cag gag tac tcg cag gaa gct tct gtt tta gtt ggt gat      192
Arg Phe Lys Gln Glu Tyr Ser Gln Glu Ala Ser Val Leu Val Gly Asp
    50                  55                  60

att aaa gtt ttg ctt atg gac agc cag gac aag tat ttt gaa gcg aca      240
Ile Lys Val Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr
65                  70                  75                  80

caa act gtt tat gaa tgg tgt ggt gtc gtg acg caa tta ctc tca gcg      288
Gln Thr Val Tyr Glu Trp Cys Gly Val Val Thr Gln Leu Leu Ser Ala
                85                  90                  95

tat att tta cta ttt gat gaa tat aat gag aaa aaa gca tca gcc cag      336
Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Gln
            100                 105                 110

aaa gac att ctc att agg ata tta gat gat ggt gtc aag aaa ctg aat      384
Lys Asp Ile Leu Ile Arg Ile Leu Asp Asp Gly Val Lys Lys Leu Asn
        115                 120                 125

gaa gcg caa aaa tct ctc ctg aca agt tca caa agt ttc aac aac gct      432
Glu Ala Gln Lys Ser Leu Leu Thr Ser Ser Gln Ser Phe Asn Asn Ala
    130                 135                 140

tcc gga aaa ctg ctg gca tta gat agc cag tta act aat gat ttt tcg      480
Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr Asn Asp Phe Ser
145                 150                 155                 160

gaa aaa agt agt tat ttc cag tca cag gtg gat aga att cgt aag gaa      528
Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Arg Ile Arg Lys Glu
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gct tat gcc ggt gct gca gcc ggc ata gtc gcc ggt ccg ttt gga tta      576
Ala Tyr Ala Gly Ala Ala Ala Gly Ile Val Ala Gly Pro Phe Gly Leu
            180                 185                 190

att att tcc tat tct att gct gcg ggc gtg att gaa ggg aaa ttg att      624
Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Ile Glu Gly Lys Leu Ile
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cca gaa ttg aat aac agg cta aaa aca gtg caa aat ttc ttt act agc      672
Pro Glu Leu Asn Asn Arg Leu Lys Thr Val Gln Asn Phe Phe Thr Ser
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tta tca gct aca gtg aaa caa gcg aat aaa gat atc gat gcg gca aaa      720
Leu Ser Ala Thr Val Lys Gln Ala Asn Lys Asp Ile Asp Ala Ala Lys
225                 230                 235                 240

ttg aaa tta gcc act gaa ata gca gca att ggg gag ata aaa acg gaa      768
Leu Lys Leu Ala Thr Glu Ile Ala Ala Ile Gly Glu Ile Lys Thr Glu
                245                 250                 255

acc gaa aca acc aga ttc tac gtt gat tat gat gat tta atg ctt tct      816
Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp Leu Met Leu Ser
            260                 265                 270

tta tta aaa gga gct gca aag aaa atg att aac acc tgt aat gaa tac      864
Leu Leu Lys Gly Ala Ala Lys Lys Met Ile Asn Thr Cys Asn Glu Tyr
        275                 280                 285

caa caa cgt cat ggt aag aag acg ctt ttc gag gtt cct gac gtc gct      912
Gln Gln Arg His Gly Lys Lys Thr Leu Phe Glu Val Pro Asp Val Ala
    290                 295                 300

agt aaa gaa acg aac caa aag cca tat aag gaa aca tac ggc att tcc      960
Ser Lys Glu Thr Asn Gln Lys Pro Tyr Lys Glu Thr Tyr Gly Ile Ser
305                 310                 315                 320

cat att aca cgc cat gat atg ctg caa atc cct gaa cag caa aaa aat     1008
His Ile Thr Arg His Asp Met Leu Gln Ile Pro Glu Gln Gln Lys Asn
                325                 330                 335

gaa aaa tat caa gtt cct gaa ttc gat tcg tcc aca att aaa aat atc     1056
Glu Lys Tyr Gln Val Pro Glu Phe Asp Ser Ser Thr Ile Lys Asn Ile
            340                 345                 350

tct tct gca aaa ggc ctg gac gtt tgg gac agc tgg cca tta caa aac     1104
Ser Ser Ala Lys Gly Leu Asp Val Trp Asp Ser Trp Pro Leu Gln Asn
        355                 360                 365

gct gac ggc act gtc gca aac tat cac ggc tac cac atc gtc ttt gca     1152
Ala Asp Gly Thr Val Ala Asn Tyr His Gly Tyr His Ile Val Phe Ala
    370                 375                 380

tta gcc gga gat cct aaa aat gcg gat gac aca tcg att tac atg ttc     1200
Leu Ala Gly Asp Pro Lys Asn Ala Asp Asp Thr Ser Ile Tyr Met Phe
385                 390                 395                 400
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tat caa aaa gtc ggc gaa act tct att gac agc tgg aaa aac gct ggc     1248
Tyr Gln Lys Val Gly Glu Thr Ser Ile Asp Ser Trp Lys Asn Ala Gly
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cgc gtc ttt aaa gac agc gac aaa ttc gat gca aat gat tct atc cta     1296
Arg Val Phe Lys Asp Ser Asp Lys Phe Asp Ala Asn Asp Ser Ile Leu
            420                 425                 430

aaa gac caa aca caa gaa tgg tca ggt tca gcc aca ttt aca tct gac     1344
Lys Asp Gln Thr Gln Glu Trp Ser Gly Ser Ala Thr Phe Thr Ser Asp
        435                 440                 445

gga aaa atc cgt tta ttc tac act gat ttc tcc ggt aaa cat tac ggc     1392
Gly Lys Ile Arg Leu Phe Tyr Thr Asp Phe Ser Gly Lys His Tyr Gly
    450                 455                 460

aaa caa aca ctg aca act gca caa gtt aac gta tca gca tca gac agc     1440
Lys Gln Thr Leu Thr Thr Ala Gln Val Asn Val Ser Ala Ser Asp Ser
465                 470                 475                 480

tct ttg aac atc aac ggt gta gag gat tat aaa tca atc ttt gac ggt     1488
Ser Leu Asn Ile Asn Gly Val Glu Asp Tyr Lys Ser Ile Phe Asp Gly
                485                 490                 495

gac gga aaa acg tat caa aat gta cag cag ttc atc gat gaa ggc aac     1536
Asp Gly Lys Thr Tyr Gln Asn Val Gln Gln Phe Ile Asp Glu Gly Asn
            500                 505                 510

tac agc tca ggc gac aac cat acg ctg aga gat cct cac tac gta gaa     1584
Tyr Ser Ser Gly Asp Asn His Thr Leu Arg Asp Pro His Tyr Val Glu
        515                 520                 525

gat aaa ggc cac aaa tac tta gta ttt gaa gca aac act gga act gaa     1632
Asp Lys Gly His Lys Tyr Leu Val Phe Glu Ala Asn Thr Gly Thr Glu
    530                 535                 540

gat ggc tac caa ggc gaa gaa tct tta ttt aac aaa gca tac tat ggc     1680
Asp Gly Tyr Gln Gly Glu Glu Ser Leu Phe Asn Lys Ala Tyr Tyr Gly
545                 550                 555                 560

aaa agc aca tca ttc ttc cgt caa gaa agt caa aaa ctt ctg caa agc     1728
Lys Ser Thr Ser Phe Phe Arg Gln Glu Ser Gln Lys Leu Leu Gln Ser
                565                 570                 575

gat aaa aaa cgc acg gct gag tta gca aac ggc gct ctc ggt atg att     1776
Asp Lys Lys Arg Thr Ala Glu Leu Ala Asn Gly Ala Leu Gly Met Ile
            580                 585                 590

gag cta aac gat gat tac aca ctg aaa aaa gtg atg aaa ccg ctg att     1824
Glu Leu Asn Asp Asp Tyr Thr Leu Lys Lys Val Met Lys Pro Leu Ile
        595                 600                 605

gca tct aac aca gta aca gat gaa att gaa cgc gcg aac gtc ttt aaa     1872
Ala Ser Asn Thr Val Thr Asp Glu Ile Glu Arg Ala Asn Val Phe Lys
    610                 615                 620
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atg aac ggc aaa tgg tac ctg ttc act gac tcc cgc gga tca aaa atg     1920
Met Asn Gly Lys Trp Tyr Leu Phe Thr Asp Ser Arg Gly Ser Lys Met
625                 630                 635                 640

acg att gac ggc att acg tct aac gat att tac atg ctt ggt tat gtt     1968
Thr Ile Asp Gly Ile Thr Ser Asn Asp Ile Tyr Met Leu Gly Tyr Val
                645                 650                 655

tct aat tct tta act ggc cca tac aag ccg ctg aac aaa act ggc ctt     2016
Ser Asn Ser Leu Thr Gly Pro Tyr Lys Pro Leu Asn Lys Thr Gly Leu
            660                 665                 670

gtg tta aaa atg gat ctt gat cct aac gat gta acc ttt act tac tca     2064
Val Leu Lys Met Asp Leu Asp Pro Asn Asp Val Thr Phe Thr Tyr Ser
        675                 680                 685

cac ttc gct gta cct caa gcg aaa gga aac aat gtc gtg att aca agc     2112
His Phe Ala Val Pro Gln Ala Lys Gly Asn Asn Val Val Ile Thr Ser
    690                 695                 700

tat atg aca aac aga gga ttc tac gca gac aaa caa tca acg ttt gcg     2160
Tyr Met Thr Asn Arg Gly Phe Tyr Ala Asp Lys Gln Ser Thr Phe Ala
705                 710                 715                 720

cca agc ttc ctg ctg aac atc aaa ggc aag aaa aca tct gtt gtc aaa     2208
Pro Ser Phe Leu Leu Asn Ile Lys Gly Lys Lys Thr Ser Val Val Lys
                725                 730                 735

gac agc atc ctt gaa caa gga caa tta aca gtt aac aaa tag tga         2253
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Gln Val Ile Pro Trp Lys Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser
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Arg Phe Lys Gln Glu Tyr Ser Gln Glu Ala Ser Val Leu Val Gly Asp
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Ile Lys Val Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr
65                  70                  75                  80

Gln Thr Val Tyr Glu Trp Cys Gly Val Val Thr Gln Leu Leu Ser Ala
                85                  90                  95

Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Gln
            100                 105                 110

Lys Asp Ile Leu Ile Arg Ile Leu Asp Asp Gly Val Lys Lys Leu Asn
        115                 120                 125

Glu Ala Gln Lys Ser Leu Leu Thr Ser Ser Gln Ser Phe Asn Asn Ala
    130                 135                 140

Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr Asn Asp Phe Ser
145                 150                 155                 160

Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Arg Ile Arg Lys Glu
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Ala Tyr Ala Gly Ala Ala Ala Gly Ile Val Ala Gly Pro Phe Gly Leu
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Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Ile Glu Gly Lys Leu Ile
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Pro Glu Leu Asn Asn Arg Leu Lys Thr Val Gln Asn Phe Phe Thr Ser
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Leu Ser Ala Thr Val Lys Gln Ala Asn Lys Asp Ile Asp Ala Ala Lys
225                 230                 235                 240

Leu Lys Leu Ala Thr Glu Ile Ala Ala Ile Gly Glu Ile Lys Thr Glu
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Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp Leu Met Leu Ser
            260                 265                 270

Leu Leu Lys Gly Ala Ala Lys Lys Met Ile Asn Thr Cys Asn Glu Tyr
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Gln Gln Arg His Gly Lys Lys Thr Leu Phe Glu Val Pro Asp Val Ala
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Ser Lys Glu Thr Asn Gln Lys Pro Tyr Lys Glu Thr Tyr Gly Ile Ser
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His Ile Thr Arg His Asp Met Leu Gln Ile Pro Glu Gln Gln Lys Asn
                325                 330                 335

Glu Lys Tyr Gln Val Pro Glu Phe Asp Ser Ser Thr Ile Lys Asn Ile
            340                 345                 350

Ser Ser Ala Lys Gly Leu Asp Val Trp Asp Ser Trp Pro Leu Gln Asn
        355                 360                 365

Ala Asp Gly Thr Val Ala Asn Tyr His Gly Tyr His Ile Val Phe Ala
    370                 375                 380

Leu Ala Gly Asp Pro Lys Asn Ala Asp Asp Thr Ser Ile Tyr Met Phe
385                 390                 395                 400

Tyr Gln Lys Val Gly Glu Thr Ser Ile Asp Ser Trp Lys Asn Ala Gly
                405                 410                 415

Arg Val Phe Lys Asp Ser Asp Lys Phe Asp Ala Asn Asp Ser Ile Leu
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Lys Asp Gln Thr Gln Glu Trp Ser Gly Ser Ala Thr Phe Thr Ser Asp
        435                 440                 445

Gly Lys Ile Arg Leu Phe Tyr Thr Asp Phe Ser Gly Lys His Tyr Gly
    450                 455                 460

Lys Gln Thr Leu Thr Thr Ala Gln Val Asn Val Ser Ala Ser Asp Ser
465                 470                 475                 480

Ser Leu Asn Ile Asn Gly Val Glu Asp Tyr Lys Ser Ile Phe Asp Gly
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Asp Gly Lys Thr Tyr Gln Asn Val Gln Gln Phe Ile Asp Glu Gly Asn
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            500                 505                 510

Tyr Ser Ser Gly Asp Asn His Thr Leu Arg Asp Pro His Tyr Val Glu
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Asp Lys Gly His Lys Tyr Leu Val Phe Glu Ala Asn Thr Gly Thr Glu
    530                 535                 540

Asp Gly Tyr Gln Gly Glu Glu Ser Leu Phe Asn Lys Ala Tyr Tyr Gly
545                 550                 555                 560

Lys Ser Thr Ser Phe Phe Arg Gln Glu Ser Gln Lys Leu Leu Gln Ser
                565                 570                 575

Asp Lys Lys Arg Thr Ala Glu Leu Ala Asn Gly Ala Leu Gly Met Ile
            580                 585                 590

Glu Leu Asn Asp Asp Tyr Thr Leu Lys Lys Val Met Lys Pro Leu Ile
        595                 600                 605

Ala Ser Asn Thr Val Thr Asp Glu Ile Glu Arg Ala Asn Val Phe Lys
    610                 615                 620

Met Asn Gly Lys Trp Tyr Leu Phe Thr Asp Ser Arg Gly Ser Lys Met
625                 630                 635                 640

Thr Ile Asp Gly Ile Thr Ser Asn Asp Ile Tyr Met Leu Gly Tyr Val
                645                 650                 655

Ser Asn Ser Leu Thr Gly Pro Tyr Lys Pro Leu Asn Lys Thr Gly Leu
            660                 665                 670

Val Leu Lys Met Asp Leu Asp Pro Asn Asp Val Thr Phe Thr Tyr Ser
        675                 680                 685

His Phe Ala Val Pro Gln Ala Lys Gly Asn Asn Val Val Ile Thr Ser
    690                 695                 700

Tyr Met Thr Asn Arg Gly Phe Tyr Ala Asp Lys Gln Ser Thr Phe Ala
705                 710                 715                 720

Pro Ser Phe Leu Leu Asn Ile Lys Gly Lys Lys Thr Ser Val Val Lys
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<212> DNA
<213> Salmonella typhi

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